

SEQUENCE LISTING

<110> Piddington, Christopher S.
Bishop, Paul D.

<120> ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG
ZACRP2

<130> 99-08D1

<150> US 09/552,204

<151> 2000-04-19

<150> US 60/130,207

<151> 1999-04-20

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<210> 1

<211> 1161

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133)...(987)

<400> 1

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gcggagcccc gccgagagct tctttgctcc ggacgcccct ggacgtggcg ggcagccgcg 120
agggtaacca cc atg atc ccc tgg gtg ctc ctg gcc tgt gcc ctc ccc tgt 171
          Met Ile Pro Trp Val Leu Leu Ala Cys Ala Leu Pro Cys
                1             5             10

gct gct gac cca ctg ctt ggc gcc ttt gct cgc agg gac ttc cgg aaa 219
Ala Ala Asp Pro Leu Leu Gly Ala Phe Ala Arg Arg Asp Phe Arg Lys
      15             20             25

ggc tcc cct caa ctg gtc tgc agc ctg cct ggc ccc cag ggc cca ccc 267
Gly Ser Pro Gln Leu Val Cys Ser Leu Pro Gly Pro Gln Gly Pro Pro
      30             35             40             45

ggc ccc cca gga gcc cca ggg ccc tca gga atg atg gga cga atg ggc 315
Gly Pro Pro Gly Ala Pro Gly Pro Ser Gly Met Met Gly Arg Met Gly
                50             55             60

ttt cct ggc aaa gac ggc caa gat gga cac gac ggc gac cgg ggg gac 363
Phe Pro Gly Lys Asp Gly Gln Asp Gly His Asp Gly Asp Arg Gly Asp
                65             70             75

agc gga gag gaa ggt cca cct ggc cgg aca ggt aac cgg gga aag cca 411
Ser Gly Glu Glu Gly Pro Pro Gly Arg Thr Gly Asn Arg Gly Lys Pro
      80             85             90

gga cca aag ggc aaa gcc ggg gcc att ggg cgg gct ggc ccc cgt ggc 459
Gly Pro Lys Gly Lys Ala Gly Ala Ile Gly Arg Ala Gly Pro Arg Gly
      95             100             105

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ccc aag ggg gtc aac ggt acc ccc ggg aag cat ggc aca cca ggc aag 507
Pro Lys Gly Val Asn Gly Thr Pro Gly Lys His Gly Thr Pro Gly Lys
110 115 120 125

aag ggg ccc aag ggc aag aaa ggg gag cca ggc ctc cca ggc ccc tgc 555
Lys Gly Pro Lys Gly Lys Lys Gly Glu Pro Gly Leu Pro Gly Pro Cys
130 135 140

agc tgt ggc agt ggc cat acc aag tca gct ttc tcg gtg gca gtg acc 603
Ser Cys Gly Ser Gly His Thr Lys Ser Ala Phe Ser Val Ala Val Thr
145 150 155

aag agc tac cca cgg gag cgg ctg ccc atc aag ttt gac aag att ctg 651
Lys Ser Tyr Pro Arg Glu Arg Leu Pro Ile Lys Phe Asp Lys Ile Leu
160 165 170

atg aac gag ggt ggc cac tac aat gct tcc agc ggc aag ttc gtc tgc 699
Met Asn Glu Gly Gly His Tyr Asn Ala Ser Ser Gly Lys Phe Val Cys
175 180 185

ggc gtg cct ggg atc tac tac ttc acc tac gac atc acg ctg gcc aac 747
Gly Val Pro Gly Ile Tyr Tyr Phe Thr Tyr Asp Ile Thr Leu Ala Asn
190 195 200 205

aag cac ctg gcc atc ggc ctg gtg cac aac ggc cag tac cgc atc cgg 795
Lys His Leu Ala Ile Gly Leu Val His Asn Gly Gln Tyr Arg Ile Arg
210 215 220

acc ttt gat gcc aac acc ggc aac cac gat gtg gcc tca ggc tcc acc 843
Thr Phe Asp Ala Asn Thr Gly Asn His Asp Val Ala Ser Gly Ser Thr
225 230 235

atc ctg gct ctc aag cag ggt gac gaa gtt tgg ctg cag atc ttc tac 891
Ile Leu Ala Leu Lys Gln Gly Asp Glu Val Trp Leu Gln Ile Phe Tyr
240 245 250

tca gag cag aac ggg ctc ttc tat gac cct tac tgg aca gac agc ctc 939
Ser Glu Gln Asn Gly Leu Phe Tyr Asp Pro Tyr Trp Thr Asp Ser Leu
255 260 265

ttt acg ggc ttc cta atc tat gcc gac cag gat gac ccc aac gag gta 987
Phe Thr Gly Phe Leu Ile Tyr Ala Asp Gln Asp Asp Pro Asn Glu Val
270 275 280 285

tagacatgcc acggcgggtcc tccaggcagg gaacaagctt ctggacttgg gcttacagag 1047
caagacccca caactgtagg ctgggggtgg ggggtcgagt gagcggttct agcctcaggc 1107
tcacctcttc cgctcttttt tttcccttcc attaaatcca aaccttttta ttca 1161

<210> 2
<211> 285
<212> PRT
<213> Homo sapiens

<400> 2
Met Ile Pro Trp Val Leu Leu Ala Cys Ala Leu Pro Cys Ala Ala Asp
1 5 10 15
Pro Leu Leu Gly Ala Phe Ala Arg Arg Asp Phe Arg Lys Gly Ser Pro
20 25 30
Gln Leu Val Cys Ser Leu Pro Gly Pro Gln Gly Pro Pro Gly Pro Pro
35 40 45
Gly Ala Pro Gly Pro Ser Gly Met Met Gly Arg Met Gly Phe Pro Gly

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50		55		60											
Lys	Asp	Gly	Gln	Asp	Gly	His	Asp	Gly	Asp	Arg	Gly	Asp	Ser	Gly	Glu
65					70					75					80
Glu	Gly	Pro	Pro	Gly	Arg	Thr	Gly	Asn	Arg	Gly	Lys	Pro	Gly	Pro	Lys
				85						90					95
Gly	Lys	Ala	Gly	Ala	Ile	Gly	Arg	Ala	Gly	Pro	Arg	Gly	Pro	Lys	Gly
			100					105					110		
Val	Asn	Gly	Thr	Pro	Gly	Lys	His	Gly	Thr	Pro	Gly	Lys	Lys	Gly	Pro
			115					120					125		
Lys	Gly	Lys	Lys	Gly	Glu	Pro	Gly	Leu	Pro	Gly	Pro	Cys	Ser	Cys	Gly
			130			135					140				
Ser	Gly	His	Thr	Lys	Ser	Ala	Phe	Ser	Val	Ala	Val	Thr	Lys	Ser	Tyr
145					150					155					160
Pro	Arg	Glu	Arg	Leu	Pro	Ile	Lys	Phe	Asp	Lys	Ile	Leu	Met	Asn	Glu
				165					170						175
Gly	Gly	His	Tyr	Asn	Ala	Ser	Ser	Gly	Lys	Phe	Val	Cys	Gly	Val	Pro
			180					185					190		
Gly	Ile	Tyr	Tyr	Phe	Thr	Tyr	Asp	Ile	Thr	Leu	Ala	Asn	Lys	His	Leu
			195				200					205			
Ala	Ile	Gly	Leu	Val	His	Asn	Gly	Gln	Tyr	Arg	Ile	Arg	Thr	Phe	Asp
			210			215					220				
Ala	Asn	Thr	Gly	Asn	His	Asp	Val	Ala	Ser	Gly	Ser	Thr	Ile	Leu	Ala
225					230					235					240
Leu	Lys	Gln	Gly	Asp	Glu	Val	Trp	Leu	Gln	Ile	Phe	Tyr	Ser	Glu	Gln
			245						250					255	
Asn	Gly	Leu	Phe	Tyr	Asp	Pro	Tyr	Trp	Thr	Asp	Ser	Leu	Phe	Thr	Gly
			260					265					270		
Phe	Leu	Ile	Tyr	Ala	Asp	Gln	Asp	Asp	Pro	Asn	Glu	Val			
		275					280					285			

<210> 3
 <211> 244
 <212> PRT
 <213> Homo sapiens

<400> 3
Met Leu Leu Leu Gly Ala Val Leu Leu Leu Leu Ala Leu Pro Gly His
1 5 10 15
Asp Gln Glu Thr Thr Thr Gln Gly Pro Gly Val Leu Leu Pro Leu Pro
20 25 30
Lys Gly Ala Cys Thr Gly Trp Met Ala Gly Ile Pro Gly His Pro Gly
35 40 45
His Asn Gly Ala Pro Gly Arg Asp Gly Arg Asp Gly Thr Pro Gly Glu
50 55 60
Lys Gly Glu Lys Gly Asp Pro Gly Leu Ile Gly Pro Lys Gly Asp Ile
65 70 75 80
Gly Glu Thr Gly Val Pro Gly Ala Glu Gly Pro Arg Gly Phe Pro Gly
85 90 95
Ile Gln Gly Arg Lys Gly Glu Pro Gly Glu Gly Ala Tyr Val Tyr Arg
100 105 110
Ser Ala Phe Ser Val Gly Leu Glu Thr Tyr Val Thr Ile Pro Asn Met
115 120 125
Pro Ile Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp
130 135 140
Gly Ser Thr Gly Lys Phe His Cys Asn Ile Pro Gly Leu Tyr Tyr Phe
145 150 155 160
Ala Tyr His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe
165 170 175
Lys Lys Asp Lys Ala Met Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Asn
180 185 190

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Asn Val Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly
    195      200      205
Asp Gln Val Trp Leu Gln Val Tyr Gly Glu Gly Glu Arg Asn Gly Leu
    210      215      220
Tyr Ala Asp Asn Asp Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr
    225      230      235      240
His Asp Thr Asn

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<210> 4
<211> 245
<212> PRT
<213> Homo sapiens

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<400> 4
Met Asp Val Gly Pro Ser Ser Leu Pro His Leu Gly Leu Lys Leu Leu
 1      5      10      15
Leu Leu Leu Leu Leu Ala Leu Arg Gly Gln Ala Asn Thr Gly Cys
    20      25      30
Tyr Gly Ile Pro Gly Met Pro Gly Leu Pro Gly Ala Pro Gly Lys Asp
    35      40      45
Gly Tyr Asp Gly Leu Pro Gly Pro Lys Gly Glu Pro Gly Ile Pro Ala
    50      55      60
Ile Pro Gly Ile Arg Gly Pro Lys Gly Gln Lys Gly Glu Pro Gly Leu
    65      70      75      80
Pro Gly His Pro Gly Lys Asn Gly Pro Met Gly Pro Pro Gly Met Pro
    85      90      95
Gly Val Pro Gly Pro Met Gly Ile Pro Gly Glu Pro Gly Glu Gly
    100      105      110
Arg Tyr Lys Gln Lys Phe Gln Ser Val Phe Thr Val Thr Arg Gln Thr
    115      120      125
His Gln Pro Pro Ala Pro Asn Ser Leu Ile Arg Phe Asn Ala Val Leu
    130      135      140
Thr Asn Pro Gln Gly Asp Tyr Asp Thr Ser Thr Gly Lys Phe Thr Cys
    145      150      155      160
Lys Val Pro Gly Leu Tyr Tyr Phe Val Tyr His Ala Ser His Thr Ala
    165      170      175
Asn Leu Cys Val Leu Leu Tyr Arg Ser Gly Val Lys Val Val Thr Phe
    180      185      190
Cys Gly His Thr Ser Lys Thr Asn Gln Val Asn Ser Gly Gly Val Leu
    195      200      205
Leu Arg Leu Gln Val Gly Glu Glu Val Trp Leu Ala Val Asn Asp Tyr
    210      215      220
Tyr Asp Met Val Gly Ile Gln Gly Ser Asp Ser Val Phe Ser Gly Phe
    225      230      235      240
Leu Leu Phe Pro Asp
    245

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<210> 5
<211> 31
<212> PRT
<213> Artificial Sequence

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<220>
<223> Aromatic motif

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<221> VARIANT
<222> (2)...(6)
<223> Each Xaa is independently any amino acid residue.

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<221> VARIANT
 <222> (7)...(7)
 <223> Xaa is asparagine or aspartic acid.

<221> VARIANT
 <222> (8)...(11)
 <223> Each Xaa is independently any amino acid residue.

<221> VARIANT
 <222> (12)...(12)
 <223> Xaa is phenyalanine, tyrosine, tryptophan or leucine.

<221> VARIANT
 <222> (13)...(18)
 <223> Each Xaa is independently any amino acid residue.

<221> VARIANT
 <222> (20)...(24)
 <223> Each Xaa is independently any amino acid residue.

<221> VARIANT
 <222> (26)...(26)
 <223> Xaa is any amino acid residue.

<221> VARIANT
 <222> (28)...(28)
 <223> Xaa is any amino acid residue.

<221> VARIANT
 <222> (30)...(30)
 <223> Xaa is any amino acid residue.

<221> VARIANT
 <222> (31)...(31)
 <223> Xaa is phenyalanine or tyrosine.

<400> 5
 Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Phe Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Phe Xaa Xaa
 20 25 30

<210> 6
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate nucleotide primer

<221> variation
 <222> (1)...(17)
 <223> n = A, T, G or C

<400> 6
 ggngansarg tntggyt

<210> 7

<211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate nucleotide primer

<221> variation
 <222> (1)...(18)
 <223> n = A, T, G or C

<400> 7
 snggnntnta ytwytttyr 18

<210> 8
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate nucleotide primer

<221> variation
 <222> (1)...(17)
 <223> n = A, T, G or C

<400> 8
 ttydsnggnt tyytnht 17

<210> 9
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate nucleotide primer

<221> variation
 <222> (1)...(18)
 <223> n = A, T, G or C

<400> 9
 ytwyrayrbn wbnwsngg 18

<210> 10
 <211> 855
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Degenerate nucleotide sequence encoding the
 polypeptide of SEQ ID NO:2.

<221> variation
 <222> (1)...(855)
 <223> n = A, T, G or C

<400> 10
 atgathccnt gggtnytnyt ngcntgygcn ytnccntgyg cngcngaycc nytnytnngn 60
 gcnttygcnm gnmngaytt ymгнаaarggn wsnccncary tngtntgyws nytnccnggn 120

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ccncarggnc cncnnggncc nccnggngcn ccnggnccnw snggnatgat gggnmgnatg 180
ggnttyccng gnaargaygg ncargayggg caygayggng aymngngnga ywsngnggar 240
garggnccnc cnggnmgnac nggnaaymgn ggnaarccng gncnaargg naargcnggn 300
gcnathggnm gngcnggncc nmngngnccn aargngtga ayggnaacnc nggnaarcay 360
ggnaacncng gnaaraargg nccnaarggn aaraarggng arccnggnyt nccnggnccn 420
tgywsntgyg gnwsnggnca yacnaarwsn gcnttywsng tngcngtnac naarwsntay 480
ccnmnggarm gnytnccnat haarttygay aarathytna tgaaygargg nggncaytay 540
aaygcwnsnw snggnaartt ygtntgyggg gtncnggna thtaytaytt yacntaygay 600
athacnytn gnaayaarca yytngcnath ggnytngtnc ayaayggna rtaymgnath 660
mgnacnttyg aygcnaayac nggnaaycay gaygtngcnw snggnwsnac nathytnngcn 720
ytnaarcarg gngaygargt ntggytncar athtitytayw sngarcaraa yggnytnnty 780
taygayccnt aytggacnga ywsnytnnty acnggnttyy tnathtaygc ngaycargay 840
gayccnaayg argtn 855

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<210> 11
<211> 536
<212> DNA
<213> Mus musculus

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<220>
<221> CDS
<222> (1)...(360)

<221> variation
<222> (1)...(536)
<223> n = A, T, G or C

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<400> 11
atc aag ttt gac aag att ctg atg aac gag ggt ggc cac tac aac gcg 48
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1 5 10 15

tcc agt ggc aag ttc gtc tgc agc gtg ccg ggg atc tna tta cnt tta 96
Ser Ser Gly Lys Phe Val Cys Ser Val Pro Gly Ile Xaa Leu Xaa Leu
20 25 30

cct atg aca tta cgc ntg gcc aac aaa cac ctg gnc atc ggc ctg gtg 144
Pro Met Thr Leu Arg Xaa Ala Asn Lys His Leu Xaa Ile Gly Leu Val
35 40 45

cac aat ggt cag tac cgc att cgg act ttt gat gcc aac acg ggc aac 192
His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp Ala Asn Thr Gly Asn
50 55 60

cac gac gtg gcc tcg ggc tcc acc atc cta gct ctc aag gag ggt gat 240
His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala Leu Lys Glu Gly Asp
65 70 75 80

gaa gtc tgg ctg cag atc ttc tac tca gag cag aat ggc ctc ttc tac 288
Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln Asn Gly Leu Phe Tyr
85 90 95

gac cct tac tgg acc gac agc ctg ttc acc ggc ttc ctc atc tac gct 336
Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly Phe Leu Ile Tyr Ala
100 105 110

gac caa gga gac ccc aac gag gta tagacaagcc ggggttgagc cttgaggtag 390
Asp Gln Gly Asp Pro Asn Glu Val
115 120

ggactaagag tctgcgtggg tgcctggagg aagatccctc gactggggct gtggactgac 450

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aatcttggga tcttttattc ccaggcaggc ctctcttatt gctgcttaaa aaagaaatca 510
ttaaataccaa gctattgatt catcta 536

<210> 12
<211> 120
<212> PRT
<213> Mus musculus

<220>
<221> VARIANT
<222> 29
<223> Xaa is any amino acid

<221> VARIANT
<222> 31
<223> Xaa is any amino acid

<221> VARIANT
<222> 38
<223> Xaa is any amino acid

<221> VARIANT
<222> 44
<223> Xaa is any amino acid

<400> 12
Ile Lys Phe Asp Lys Ile Leu Met Asn Glu Gly Gly His Tyr Asn Ala
1 5 10 15
Ser Ser Gly Lys Phe Val Cys Ser Val Pro Gly Ile Xaa Leu Xaa Leu
20 25 30
Pro Met Thr Leu Arg Xaa Ala Asn Lys His Leu Xaa Ile Gly Leu Val
35 40 45
His Asn Gly Gln Tyr Arg Ile Arg Thr Phe Asp Ala Asn Thr Gly Asn
50 55 60
His Asp Val Ala Ser Gly Ser Thr Ile Leu Ala Leu Lys Glu Gly Asp
65 70 75 80
Glu Val Trp Leu Gln Ile Phe Tyr Ser Glu Gln Asn Gly Leu Phe Tyr
85 90 95
Asp Pro Tyr Trp Thr Asp Ser Leu Phe Thr Gly Phe Leu Ile Tyr Ala
100 105 110
Asp Gln Gly Asp Pro Asn Glu Val
115 120

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide ZC20810

<400> 13
gggcttccta atctatgc

18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC20809
 <400> 14
 tgggggtcttg ctctgtaa 18
 <210> 15
 <211> 25
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide ZC23375
 <400> 15
 gcgagggtag gatccatgat cccct 25
 <210> 16
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide ZC23376
 <400> 16
 gccgtggtct agatatacct cgt 23
 <210> 17
 <211> 7
 <212> PRT
 <213> Artificial Sequence
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 <223> Glu-Glu tag
 <400> 17
 Glu Glu Tyr Met Pro Met Glu
 1 5
 <210> 18
 <211> 17
 <212> DNA
 <213> Artificial Sequence
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 <223> Oligonucleotide ZC447
 <400> 18
 taacaatttc acacagg 17
 <210> 19
 <211> 18
 <212> DNA
 <213> Artificial Sequence
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 <223> Oligonucleotide ZC976
 <400> 19

cgttgtaaaa cgacggcc 18

<210> 20
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 <212> PRT
 <213> Artificial Sequence

<220>
 <223> purification peptide

<400> 20
 Glu Tyr Met Pro Val Asp
 1 5

<210> 21
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Representative contig

<400> 21
 atggcttagc tt 12

<210> 22
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 <212> DNA
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<220>
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<400> 22
 tagcttgagt ct 12

<210> 23
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Representative contig

<400> 23
 agccatcagc tg 12